



## AMENDMENT

### In the Specification:

Please add the below subheading and replace the paragraph under the title, on page 1, lines 4-8, with the following:

#### Cross-Reference to Related Applications

This application is a continuation-in-part application of U.S. Ser. No. 09/323,597 filed June 1, 1999 which claims the benefit of United States provisional patent application serial numbers 60/087,598, filed June 1, 1998, now lapsed, 60/091,474 filed June 29, 1998, now lapsed and 60/129,521, filed April 14, 1999, now lapsed. The entire contents of these provisional and non-provisional patent applications are incorporated by reference into this application.

Please replace the paragraph from page 16, line 32 through page 17, line 7 with the following:

In the context of amino acid sequence comparisons, the term "identity" is used to express the percentage of amino acid residues at the same relative positions that are the same. Also in this context, the term "homology" is used to express the percentage of amino acid residues at the same relative positions that are either identical or are similar, using the conserved amino acid criteria of BLAST analysis, as is generally understood in the art. For example, % identity values may be generated by WU-BLAST-2 (Altschul et al., 1996, Methods in Enzymology 266:460-480; available at [http address "blast.wustl.edu/blast/README.html"](http://blast.wustl.edu/blast/README.html)). Further details regarding amino acid substitutions, which are considered conservative under such criteria, are provided below.

**Please replace the paragraph from page 31, lines 21-31 with the following:**

Redundancy in the genetic code permits variation in 20P1F12/TMPRSS2 gene sequences. In particular, one skilled in the art will recognize specific codon preferences by a specific host species and can adapt the disclosed sequence as preferred for a desired host. For example, preferred codon sequences typically have rare codons (i.e., codons having a usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific organism may be calculated, for example, by utilizing codon usage tables available on the Internet at the following address: “[www.dna.affrc.go.jp/~nakamura/codon.html](http://www.dna.affrc.go.jp/~nakamura/codon.html).” Nucleotide sequences that have been optimized for a particular host species by replacing any codons having a usage frequency of less than about 20% are referred to herein as “codon optimized sequences.”

**In the Claims:**

Please amend the claims as follows:

Please cancel claims 4, 8-9, 14, 16, 20-28 and 39-47.

**Please replace the presently pending claims with the following claims:**

1. (Twice amended) A method of examining a biological sample for evidence of tumor cell growth comprising comparing the expression level of the 20P1F12/TMPRSS2 gene, which encodes the protein of SEQ. ID. NO: 2 (Figure 1), in the biological sample to the expression of said 20P1F12/TMPRSS2 gene in a corresponding normal sample, wherein enhancement of the level of 20P1F12/TMPRSS2 expression in the biological sample is evidence of tumor cell growth.
2. (Amended) The method according to claim 1, wherein the level of expression of the 20P1F12/TMPRSS2 gene in the biological sample is evaluated by examining the level of 20P1F12/TMPRSS2 protein produced.